

FIG.1A

GAGCTCGGAT	CCACTACTCG	ACCCACGCGT	CCGGCCAGGA	CCTCTGTGAA	CCGGTCGGGG	60
CGGGGGCCGC	CTGGCCGGGA	GTCTGCTCGG	CGGTGGGTGG	CCGAGGAAGG	GAGAGAACGA	120
TCGCGGAGCA	GGGCGCCCGA	ACTCCGGGCG	CCGGCC	ATG CGC CGG GCC AGC CGA		175
				Met Arg Arg Ala Ser Arg		
				1	5	
GAC TAC GGC AAG	TAC CTG CGC AGC	TCG GAG GAG	ATG GGC AGC GGC CCC			223
Asp Tyr Gly Lys	Tyr Leu Arg Ser	Glu Glu Met Gly	Ser Gly Pro			
	10	15	20			
GGC GTC CCA CAC	GAG GGT CCG CTG CAC	CCC GCG CCT	TCT GCA CCG GCT			271
Gly Val Pro His	Glu Gly Pro Leu	His Pro Ala Pro	Ala Pro Ala			
	25	30	35			

FIG.1B

CCG GCG CCG CCA CCC GCC GTC TCC CGC TCC ATG TTC CTG GCC CTC CTG	319
Pro Ala Pro Pro Ala Ala Ser Arg Ser Met Phe Leu Ala Leu Leu	
40 45 50	
GGG CTG GGA CTG GGC CAG GTG GTC TGC AGC ATC GCT CTG TTC CTG TAC	367
Gly Leu Gly Leu Gly Gln Val Val Cys Ser Ile Ala Leu Phe Leu Tyr	
55 60 65 70	
TTT CGA GCG CAG ATG GAT CCT AAC AGA ATA TCA GAA GAC AGC ACT CAC	415
Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser Glu Asp Ser Thr His	
75 80 85	
TGC TTT TAT AGA ATC CTG AGA CTC CAT GAA AAC GCA GGT TTG CAG GAC	463
Cys Phe Tyr Arg Ile Leu Arg Leu His Glu Asn Ala Gly Leu Gln Asp	
90 95 100	
TCG ACT CTG GAG AGT GAA GAC ACA CTA CCT GAC TCC TGC AGG AGG ATG	511
Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro Asp Ser Cys Arg Arg Met	
105 110 115	

FIG.1C

AAA CAA GCC TTT CAG GGG GCC GTG CAG AAG GAA CTG CAA CAC ATT GTG	559
Lys Gln Ala Phe Gln Gly Ala Val Gln Lys Glu Leu Gln His Ile Val	
120 125 130	
GGG CCA CAG CGC TTC TCA GGA GCT CCA GCT ATG ATG GAA GGC TCA TGG	607
Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala Met Met Glu Gly Ser Trp	
135 140 145 150	
TTG GAT GTG GCC CAG CGA GGC AAG CCT GAG GCC CAG CCA TTT GCA CAC	655
Leu Asp Val Ala Gln Arg Gly Lys Pro Glu Ala Gln Pro Phe Ala His	
155 160 165	
CTC ACC ATC AAT GCT GCC AGC ATC CCA TCG GGT TCC CAT AAA GTC ACT	703
Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser Gly Ser His Lys Val Thr	
170 175 180	

FIG.1D

CTG TCC TCT TGG TAC CAC GAT CGA GGC TGG GCC AAG ATC TCT AAC ATG	751
Leu Ser Ser Trp Tyr His Asp Arg Gly Trp Ala Lys Ile Ser <u>Asn</u> Met	
185	190
ACG TTA AGC AAC GGA AAA CTA AGG GTT AAC CAA GAT GGC TTC TAT TAC	799
Thr Leu Ser Asn Gly Lys Leu Arg Val Asn Gln Asp Gly Phe Tyr Tyr	
200	205
CTG TAC GCC AAC ATT TGC TTT CGG CAT CAT GAA ACA TCG GGA AGC GTA	847
Leu Tyr Ala Asn Ile Cys Phe Arg His His Glu Thr Ser Gly Ser Val	
215	220
CCT ACA GAC TAT CTT CAG CTG ATG ATG GTG TAT GTC GTT AAA ACC AGC ATC	895
Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr Val Val Lys Thr Ser Ile	
	235
	240
	245

FIG.1E

AAA ATC CCA AGT TCT CAT AAC CTG ATG AAA GGA GGG AGC ACG AAA AAC	943
Lys Ile Pro Ser Ser His Asn Leu Met Lys Gly Gly Ser Thr Lys <u>Asn</u>	
250 255 260	
TGG TCG GGC AAT TCT GAA TTC CAC TTT TAT TCC ATA AAT GTT GGG GGA	991
Trp Ser Gly Asn Ser Glu Phe His Phe Tyr Ser Ile Asn Val Gly Gly	
265 270 275	
TTT TTC AAG CTC CGA GCT GGT GAA GAA ATT AGC ATT CAG GTG TCC AAC	1039
Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile Ser Ile Gln Val Ser <u>Asn</u>	
280 285 290	
CCT TCC CTG CTG GAT CCG GAT CAA GAT GCG ACG TAC TTT GGG GCT TTC	1087
Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala Thr Tyr Phe Gly Ala Phe	
295 300 305 310	
AAA GTT CAG GAC ATA GAC T GAGACTCATT TCGTGGAACA TTAGCATGGA	1136
Lys Val Gln Asp Ile Asp	
315	

FIG.1F

TGTCCTAGAT	GTTTGGAAAC	TTCTTAAAAA	ATGGATGATG	TCTATACATG	TGTAAGACTA	1196
CTAAGAGACA	TGGCCCCACGG	TGTATGAAAC	TCACAGCCCT	CTCTCTTGAG	CCTGTACAGG	1256
TTGTGTATAT	GTAAGTCCA	TAGTGATGT	TAGATTTCATG	GTGATTACAC	AACGGTTTAA	1316
CAATTTTGTA	ATGATTTCCCT	AGAATTGAAC	CAGATTGGGA	GAGGTATTCC	GATGCTTATG	1376
AAAAACTTAC	ACGTGAGCTA	TGGAAGGGGG	TCACAGTCTC	TGGGTCTAAC	CCCTGGACAT	1436
GTGCCACTGA	GAACCTTGAA	ATTAAGAGGA	TGCCATGTCA	TTGCAAAGAA	ATGATAGTGT	1496
GAAGGGTTAA	GTTCTTTTGA	ATTGTTACAT	TGCGCTGGGA	CCTGCAAATA	AGTCTTTTIT	1556

FIG.1G

TTCTAATGAG GAGAGAAAAA TATATGTATT TTTATATAAT GTCTAAAGTT ATATTCAGG	1616
TGTAATGTTT TCTGTGCAA GTTTGTAAA TTATATTTGT GCTATAGTAT TTGATTCAAA	1676
ATATTTAAAA ATGTCTCACT GTTGACATAT TTAATGTTTT AAATGTACAG ATGTATTAA	1736
CTGGTGCACT TTGTAATTCC CCTGAAGGTA CTCGTAGCTA AGGGGCAGA ATACTGTTTC	1796
TGGTGACCAC ATGTAGTTTA TTTCTTTATT CTTTTTAACT TAATAGAGTC TTCAGACTTG	1856
TCAAAACTAT GCAAGCAAAA TAAATAAATA AAAATAAAAT GAATACCTTG AATAATAAGT	1916
AGGATGTTGG TCACCAGGTG CCTTTCAAAT TTAGAAGCTA ATTGACTTTA GGAGCTGACA	1976
TAGCCAAAAA GGATACATAA TAGGCTACTG AAATCTGTCA GGAGTATTTA TGCAATTATT	2036

FIG.1H

GAACAGGTGT	CTTTTTTAC	AAGAGCTACA	AATGTAAAT	TTTGTTTCTT	TTTTTTCCCA	2096
TAGAAAATGT	ACTATAGTTT	ATCAGCCAAA	AAACAATCCA	CTTTTAAAT	TAGTAAAGT	2156
TATTTTATTA	TACTGTACAA	TAAAAGCATT	GTCTCTGAAT	GTTAATTTTT	TGTTACAAAA	2216
AAATAAATTG	TACGAAAACC	TGAAAAAAA	AAAAAAA	AAAAAAGGG	CGCCGCTCT	2276
AGAGGGCCCT	ATTCTATAG					2295

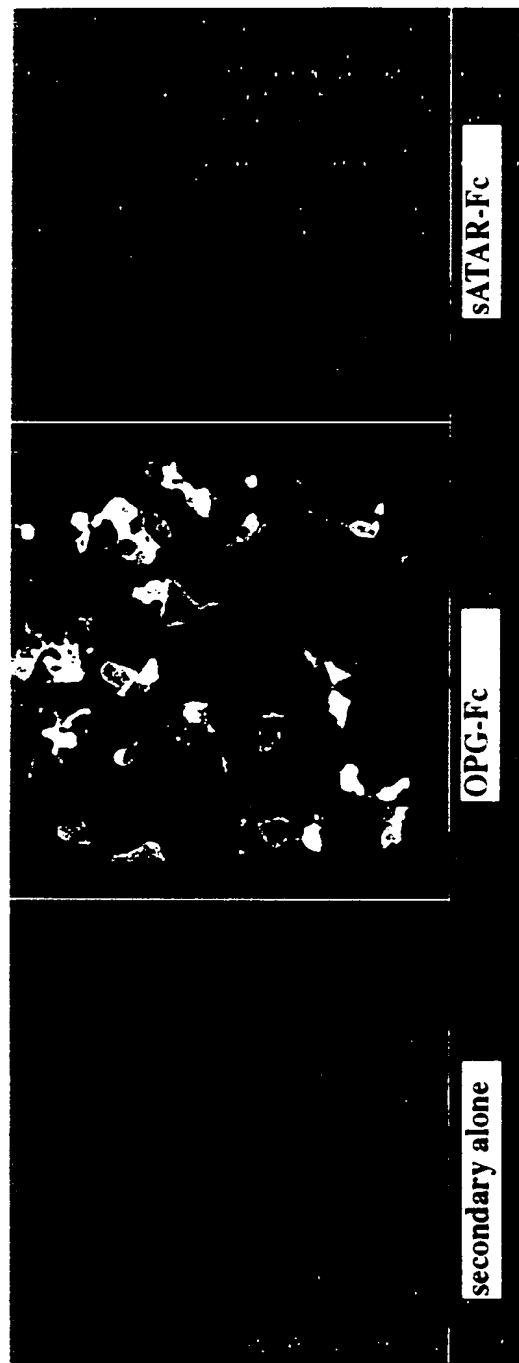


FIG. 2

9.5 kb —
7.5 kb —
4.4 kb —
2.4 kb —
1.4 kb —

Thymus
Prostate
Testis
Ovary
Small Intestine
Colon

Spleen
Lymph Node
Thymus
PBL
Bone Marrow
Fetal Liver

9.5 kb —
7.5 kb —
4.4 kb —
2.4 kb —
1.4 kb —



FIG. 3